Mapping Quantitative Trait Loci Associated with Resistance to Coccidiosis and Growth

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ABSTRACT To map QTL associated with disease resistance to avian coccidiosis and growth, two commercial broiler lines with different degrees of resistance to the disease were crossed to generate an F_1 generation that was intercrossed to produce 314 F_2 generation offspring. The F_2 offspring were inoculated with sporulated oocysts of *Eimeria maxima*. Five disease-associated phenotypes were measured after the infection. Intertrait comparisons revealed that oocyst shedding was a good parameter for evaluating disease resistance or susceptibility. One hundred nineteen microsatellite markers, covering 80% of the chicken genome with an average marker interval of 25 cM, were used for genotyping of F_1 parents and F_2 offspring. Statistical analysis based on the data of four families revealed a locus on chromosome 1 associated with oocyst shedding (logarithm of odds = 3.46). The genetic mechanism of this locus appeared additive. The genomic scan also identified three potential growth QTL on chromosomes 1, 6, and 8. These results provide the foundation for further investigation to validate the QTL.

(*Key words*: QTL, disease resistance, coccidiosis, growth, chicken)

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INTRODUCTION

Avian coccidiosis is an infectious disease caused by several distinct species of *Eimeria* parasites. The parasites infect the chicken digestive tract, and disease caused by the infection significantly retards growth. The current strategies of disease control are prophylactic medication and vaccination. However, the wide variety of *Eimeria* strains and continual emergence of drug-resistant strains limit the effectiveness of both methods. An alternative approach to control coccidiosis is to breed chickens resistant to the disease.

There is evidence of genetic variation associated with resistance or susceptibility to avian coccidiosis. Experiments by Champion (1953) and Rosenberg et al. (1953) demonstrated genetic factors influencing resistance to avian coccidiosis, and the genetic influence appeared to be additive and not sex linked. The heritability estimates for BW gain and packed cell volume in infected chickens were 0.20 and 0.30, respectively (Mathis et al., 1984). Selection of White Leghorns for resistance and susceptibility to avian coccidiosis resulted in a sixfold difference in mortality rates between these selected lines (Johnson and Edgar, 1982).

Because chickens show different degrees of sickness after infection with *Eimeria*, resistance or susceptibility to coccidiosis can be considered a quantitatively inherited trait, most likely controlled by multiple genes. Unlike many production traits, however, the methods of assessing coccidiosis severity are not well established. Historically, BW gain, intestinal lesion score, feed conversion, plasma constituents, and oocyst shedding have been measured in chickens from established genetic lines inoculated with equal number of oocysts to determine resistance or susceptibility status (Martin et al., 1986; Lillehoj and Ruff, 1987; Lillehoj et al., 1989; Bumstead and Millard, 1992; Conway et al., 1993; Nakai et al., 1993; Allen, 1997; Caron et al., 1997; Allen and Lillehoj, 1998; Pinard-Van Der Laan et al., 1998). However, these measurements were only weakly correlated among themselves (Bumstead and Millard, 1987; Caron et al., 1997; Idris et al., 1997; Zhu et al., 2000), and a single trait constituting the best indicator of disease resistance remains to be determined.

Technical difficulties hamper attempts to breed disease-resistant chickens by traditional selection approaches. The

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Abbreviation Key: LOD = logarithm of odds; PI = post-inoculation; SOLAR = Sequential oligogenic linkage analysis.

DNA marker technologies offer an alternative, efficient means to facilitate this process. Using DNA marker techniques, QTL controlling the trait of interest can be identified and used in marker-assisted selection. Currently, 1,889 DNA-based genetic markers are available for chicken genotyping, 480 of which have been assigned to 50 linkage groups (Groenen et al., 2000). These markers have been applied to inbred and outbred populations to identify QTL affecting growth, feed efficiency, and carcass traits (Groenen et al., 1997; Van Kaam et al., 1998, 1999a,b; Tatsuda and Fujinaka, 2001), as well as resistance to Marek's disease and antibody production (Vallejo et al., 1998; Xu et al., 1998; Yonash et al., 1999, 2001).

Several challenges confront the use of outbred resource populations for QTL mapping (Ver der Beek et al., 1995; Lynch and Walsh, 1998). Most of all, linkage phases between genes underlying quantitatively measured traits and linked markers, as well as the informativeness of marker loci, may vary among families. Parents with identical alleles at marker loci may not necessarily possess identical QTL alleles controlling a given trait. Therefore, the association between markers and traits must be evaluated separately for each family. One approach to increase informative families is using crosses between populations widely different in traits of interest and subsequent intercrossing of the F_1 to generate the F_2 or backcrossing F_1 to the parental lines (Soller and Andersson, 1998).

Several statistical methods have been developed to detect QTL in outbred populations (Hoeschele et al., 1997). Interval linkage analysis, originally based on identity by descent of alleles shared between pairs of relatives (Haseman and Elston, 1972), has been improved with multipoint linkage analysis (Fulker et al., 1995; Kruglyak and Lander, 1995) and variance-component linkage analysis (Goldgar, 1990; Schork, 1993; Amos, 1994; Blangero and Almasy, 1997). It has been demonstrated that variance-component linkage analysis is more powerful than the relative pair-based approach (Shurgart and Goldgar, 1999). In current study, whole genome scanning with microsatellite markers and variance-component linkage analysis were performed to identify QTL associated with growth and resistance to avian coccidiosis in commercial broiler chickens.

MATERIALS AND METHODS

Resource Populations

Two parental broiler lines (sire and dam) were used as resource populations for the present study. Both lines have undergone at least 20 generations of selection for a variety of production traits. Substantial differences in resistance to coccidiosis and Marek's disease have been noted between these lines (Emara et al., 2002). The study reported here was based on the design of a two generation, full-sib family pedigree as described by Van der Beek et al. (1995). Thirty male and 100 female chickens from these sire and dam lines, respectively, were crossed to produce F_1 chickens. Eighteen randomly selected pairs of F_1 males and females were selected to generate an F_2 population. Twelve pairs with the highest egg production in the first hatch were chosen as the F_1 of the resource population. A total of 314 F_2 offspring in the 12 full-sib families were obtained from four hatches. The family sizes ranged from 10 to 44. Pedigree information was recorded, and all birds were traced with wing bands attached at hatching.

Phenotypic Measurement of Disease Susceptibility

The F_2 chickens from different families were mixed and raised in the same room of a specific pathogen-free housing facility according to guidelines established by the Agricultural Research Service, U.S. Department of Agriculture. At 4 wk of age, the chickens were transferred to a disease challenge facility and randomly assigned to individual cages. Chickens with overt signs of disease prior to *Eimeria* challenge were excluded from the study. Animals were orally inoculated with an optimized dose (1×10^4) of sporulated *E. maxima* oocysts on Day 0 as described (Zhu et al., 2000). Body weight was measured on Days 0, 3, 6, and 9 post-infection (PI). One fecal sample per bird was collected between Days 5 to 9 PI, and the number of oocysts was evaluated by the method of Lillehoj and Ruff (1987). Blood samples were collected in sodium EDTA on Days 0, 3, 6, and 9 PI for measurement of plasma interferon (IFN)-γ by enzyme-linked immunosorbent assay as described (Yun et al., 1999) and $NO_2^- + NO_3^-$ and carotenoid by the chemical protocols described by Allen (1997).

Marker Genotyping

Genotyping was performed by PCR using microsatellite markers provided by the United States Poultry Coordinators, National Animal Research Program. The PCR was performed as described previously (Cheng and Crittenden, 1994) with modifications. Genomic DNA used for genotyping was extracted from blood cells by the method of Zhu et al. (1995). For the current study, a 10-μL PCR reaction contained 100 to 200 ng of genomic DNA, 100 to 500 nM of each primer, and 1.8 mM of $MgCl_2$. Initially, the twenty-four F_1 chickens were genotyped using one marker per PCR reaction. The genotypic data were used to develop multiplex PCR (two to six markers) for genotyping F_2 progeny. The PCR reactions were diluted 5- to 20-fold with sterile H_2O depending on amplification efficiency. One microliter of the reaction was mixed with 9.7 μL of formaldehyde and 0.3 μL of HD400 ROX DNA size standards[3] for genotyping with an ABI 3700 sequencer.[3] In some experiments, 1.0 μL of the diluted PCR sample was mixed with 2.0 μL of formaldehyde and 0.5 μL of GeneScan-350 TAMRA size standards[3] for genotyping with an ABI 373 sequencer.[3] All sample mixtures were heated at 95 C for 5 min before analysis. Allele scoring was performed using Genotyper software, Versions 2.5 and 3.5.[3]

[3]Applied Biosystem Corp., Foster City, CA.

Statistical Analysis of Phenotypic Data

To identify covariates, the data were analyzed with SAS Proc GLM software[4] using the model $Y_{ijk} = \mu + h_i + s_j + h \times s_{(ij)} + \varepsilon_{ijk}$, where Y_{ijk} is observation k in hatch i and sex j, μ is the population mean, h_i is the effect of hatch i, s_j is the effect of sex j, $h \times s_{(ij)}$ is the interaction between hatch and sex, and ε_{ijk} is a random residual. If the covariates were significant ($P < 0.05$), the residual of the statistical model containing the significant covariates were re-analyzed with the univariate procedure to test normality of the trait distribution. The data were transformed if normality was invalid ($P < 0.05$). The data adjusted for these effects; i.e., the residuals of the statistical model were used to estimate correlations among the traits.

Linkage Analysis

Location of the markers on the consensus chicken genetic linkage map (Groenen et al., 1998, 2000) was used as the criterion to select 119 microsatellite markers for analysis. Of 119 markers in the study, 16 linkage groups were represented by a single marker per group. If the unlinked markers covered 20 cM, and 3,500 cM of the genome were assumed, the 119 markers covered approximately 80% of the genome. Based on the chicken consensus map, the average interval between linked markers in current study was 25 cM.

Genotypic data collected from F_1 and F_2 chickens of the 12 full-sib families were tested for Mendelian inheritance within the families to verify parentage. The data were then analyzed with CRI-MAP[5] to test the agreement of the linkage map of these families with the consensus chicken linkage map. The mapping function of Kosambi (1944) was used to transform the recombination fraction to genetic distance between linked markers. A minimal logarithm of odds (LOD) score of 3.0 was used as the significant threshold for declaring linkage (Hu et al., 1997).

QTL Analysis

Sequential oligogenic linkage analysis[6] (SOLAR) was used to perform QTL linkage analysis. Variance-component-based multipoint quantitative-trait linkage analysis was implemented in the package according to methods reported by Almasy and Blangero (1998). The program was modified to allow analysis of linkage groups larger than 500 cM. The F_1 and F_2 genotypes and F_2 phenotypes were used in the QTL linkage analysis. Hatch and sex were included in the statistical models as covariates if these factors were significant ($P \leq 0.1$). Maximum likelihood estimates for allelic frequencies were used to input genotypes of missing data, and marker-specific identity by descent matrices were calculated according to the Curtis and Sham algorithm that was implemented in the software package. Single- and multipoint analyses were performed.

The threshold of significance was based on the guidelines suggested for genome scans with different marker intervals by Lander and Kruglyak (1995). Based on the number of markers used in current experiment, the LOD score significance threshold for single marker analysis was reduced by 25% of the suggested LOD score (3.6) for a genomic scan with markers spacing every 0.1 cM. Therefore, the significant LOD score was 2.7 for single-point linkage analysis in the present experiment. Multipoint linkage analysis of linked markers was carried out with an increment of 1 cM if single-point analysis yielded LOD scores larger than 1.0 in a linkage group. The significance threshold of LOD scores for the multipoint analysis at 1-cM marker intervals was reduced by 7% of the LOD score 3.6 according the guidelines, or 3.35.

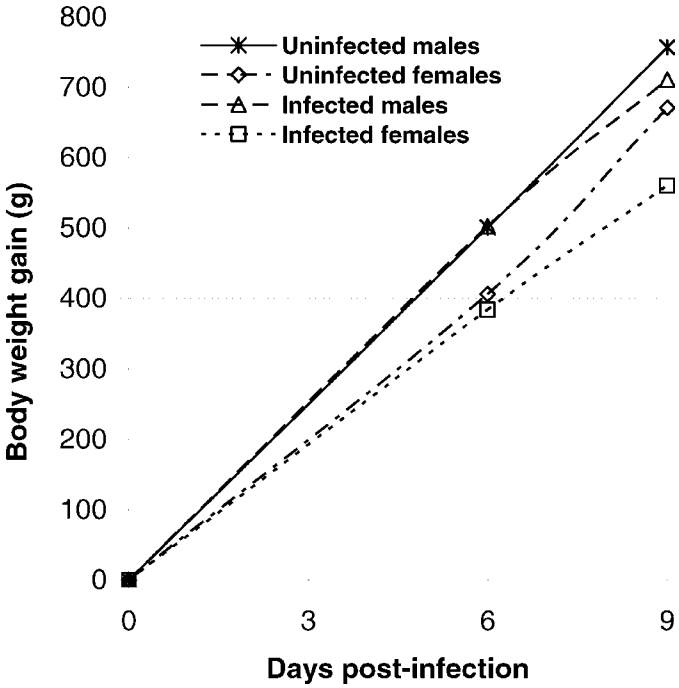

FIGURE 1. Body weight gains of *Eimeria* infected male and female chickens at Days 6 and 9 post-infection and non-infected chickens at the same ages.

RESULTS

Analysis of F_2 Phenotypes

Sex effect was highly significant ($P < 0.001$) for BW measurements across all time periods, and hatch effect was significant for oocyst shedding, $NO_2^- + NO_3^-$, carotenoid, and IFN-γ concentrations. Sex and hatch interactions were significant only for $NO_2^- + NO_3^-$ and IFN-γ concentrations. Distributions of all measured traits except oocyst shedding were normal after covariate adjustment. The data of oocyst shedding appeared to be normally distributed after square-

[4]SAS Release 6.12, SAS Institute, Inc., Cary, NC.

[5]Green, P., K. Falls, and S. Crooks. Documentation for CRI-MAP Version 2.4 (March 26, 1990). http://linkage.rockefeller.edu/soft/crimap/.

[6]Version 1.6.6, Southwest Foundation for Biomedical Research, San Antonio, TX.

TABLE 1. Correlation coefficients between oocyst shedding and other coccidiosis-associated traits measured from *Eimeria*-infected chickens

Trait[1]	Females	Males
BW0	0.07	0.01
BWG09	–0.25	–0.06
BWG39	–0.43*	–0.18
BWG69	–0.57*	–0.16
GR69	–0.62*	–0.16
Plasma carotenoid[2]	0.57*	0.64*
Plasma NO^{2-} + NO_3^-	0.22	0.02
Plasma interferon-γ	0.16	0.11

[1]BW0 = body weight at time of challenge; BWG09 = body weight gain between Days 0 and 9 post-infection (PI), BWG39 = body weight gain between Days 3 and 9 PI; BWG69 = body weight gain between Days 6 and 9 PI; and GR69 = growth rate between Days 6 and 9 PI.

[2]Difference in plasma carotenoid concentrations between Days 3 and 9 PI.

*Significantly different from 0 ($P < 0.05$).

root transformation. All phenotypic values were adjusted using significant covariates and expressed as residuals. Transformed or covariate-adjusted data were used in the statistical analysis of disease susceptibility and QTL mapping.

Assessment of Disease Susceptibility

Five parameters were measured after *Eimeria* infection to indicate the individual status of genetic resistance to avian coccidiosis. There were not differences between infected and infected chickens in BW gain PI for males and females, though growth retardation due to coccidiosis appeared to be much greater in females than in males, accounting for 33.6 and 18.6% of BW gain of uninfected birds between Day 6 and Day 9 PI and only 7 and 2.7 % of the BW, respectively (Figure 1).

Correlation between oocyst shedding and other measurements indicated that oocyst shedding was probably a better indicator of disease susceptibility. Oocyst shedding was not correlated to BW at time of *Eimeria* challenge in males and females, but it was significantly correlated to the weight gain after Day 3 PI in females (Table 1). the correlation coefficients increased as the period considered was shifted to later days of the infection. In males, no significant correlations were observed between oocyst shedding and BW associated parameters. The differences in plasma carotenoid concentration between Days 3 and 9 were significantly correlated with oocyst shedding in both males and females. The differences in carotenoid concentration also displayed a significant correlation (r = –0.29) to BW gain between Days 6 and 9, but the correlation coefficient was much smaller than that between oocyst shedding and BW gain between Days 6 and 9 (r = –0.57) in females. Two parameters, NO_2^- + NO_3^- and IFN-γ, did not show significant correlation with other parameters.

Genetic Linkage Analysis

One F_2 chicken was found to have incorrectly identified parentage based on genotypic data, and four F_1 chickens with missed wing bands were placed in families based on pedigree records and genotypes. Four markers displayed null alleles (no PCR products) according to the segregation patterns of marker alleles. If the genotypes could not be determined due to null alleles, the genotypes were considered as missing. The average heterozygosity of F_1 at marker loci was 68.1% (Table 2). Heterozygosity at the loci on chromosome Z was lowest (54%) of all linkage groups. The values ranged from 58 to 84%.

Linkage analysis of the markers based on the F_1 and F_2 genotypes yielded results very similar to the chicken consensus genetic linkage map. The orders of the markers on the chromosomes were identical to the consensus map, but genetic distances between some markers appeared to be slightly larger than those in the consensus map. For the markers that were distantly linked to other selected markers based on the consensus map, the linkages were not significant (LOD < 3) in the linkage analysis. Consensus locations of 119 markers were used in multipoint linkage analysis.

TABLE 2. Linkage groups, marker coverage, marker intervals, and heterozygosity of F_1 at the selected marker loci

Linkage groups	Ranges of marker coverage (cM)[1]	Number of markers	Average marker intervals (cM)	Heterozygosity (%)
Chromosome 1	33–518	23	22	69.9
Chromosome 2	6–403	16	26	67.5
Chromosome 3	0–317	12	29	78.1
Chromosome 4	0–243	10	27	63.3
Chromosome 5	32–198	8	24	63.5
Chromosome 6	31–126	6	19	71.7
Chromosome 7	0–165	4	51	84.4
Chromosome 8	26–94	4	17	58.0
Chromosome Z	20–160	8	20	54.2
E29C09W09	48–107	4	20	69.8
E35C18W14	0–72	3	36	76.4
E41W17	26–57	3	16	75.0
E59C35W20	11–59	4	16	63.5
Others (1 per group)	N/A	15	N/A	65.6
Summary	Total[2] = 2,826	Total = 119	Average = 25	Average = 68.1

[1]Linkage map positions of starting and ending markers on the linkage groups.

[2]Markers that did not link to other markers are assumed to cover 20 cM of chromosomal regions.

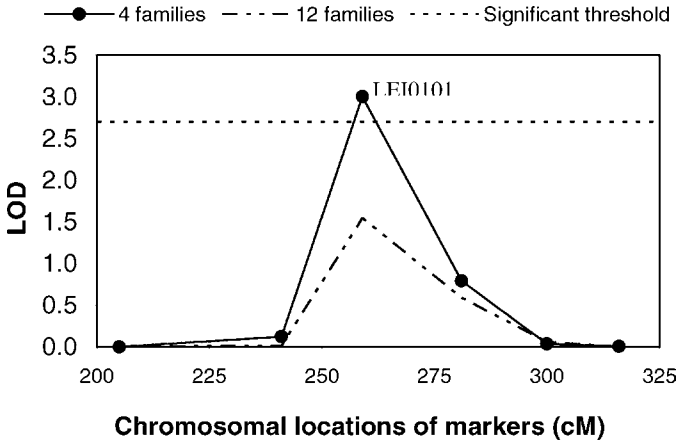

FIGURE 2. Logarithm of odds scores (LOD) of single-point linkage analysis based on oocyst shedding and six markers covering approximate 100 cM on chromosome 1.

QTL Analysis

Oocyst shedding was considered as the phenotype for resistance to avian coccidiosis, whereas BW at the end of the experiment (37 d of age) was the phenotype for growth. The phenotypes of these two traits were included in the QTL detection analysis to locate QTL associated with these traits. Chickens of the last hatch did not show acceptable infection level based on oocyst shedding and were not included in analysis of QTL associated with this trait. Hatch and sex were the significant effects for oocyst shedding and body weight gain between inoculation and Day 9 PI, respectively; therefore, these two factors were included in the statistical models to account for these effects before analysis with SOLAR. Hatch effect accounted for 21.2% of total variance of oocyst shedding, whereas sex contributed 24.8 % to the total BW variation.

Using single-point analysis of association with oocyst shedding, the LOD scores at all marker loci were less than 0.5, except for LEI0101 (259 cM on chromosome 1). This marker displayed a LOD score of 1.55 in the single-point linkage analysis (Figure 2). Multipoint analysis yielded a very similar result. To identify non-informative families at this potential QTL, multipoint linkage analysis was conducted based on each single family. Eight families displayed zero heritability due to the chromosomal region (40 cM) of LEI0101. If these eight families were assumed non-informative at this potential QTL and were excluded, the LOD score at LEI0101 increased to 3.02 for single point analysis based on the rest of four families (Figure 2). The heritability associated with the marker locus increased from 0.14 to 0.39. Multipoint linkage analysis with 1 cM increments revealed that the highest peak with a LOD score of 3.46 on chromosome 1 was located at 252 cM (Figure 3). The heritability associated with this locus based on the four families increased to 0.54.

To examine the genetic effect at the QTL, linkage disequilibrium within families was used to associate the detected locus with the linked marker locus, LEI0101. The F_2 offspring of the largest family were divided into four groups based on their marker genotypes at LEI0101, 1/3, 2/3, 1/2, and 2/2 inherited from their parents with marker genotypes of 1/2 and 2/3. Alleles 2 in both parents were assumed to be identical. Figure 4 shows that the genetic effect at this locus appeared additive by comparing the means of oocyst shedding of different genotypes. The differences among genotypes were highly significant. It appeared that Allele 3 had the largest genetic effect and Allele 1 had the smallest effect. Allele 3 was responsible for the low oocyst shedding, whereas Allele 2 contributed to the high shedding. Allele 1 displayed a medium effect on the oocyst shedding. The other three smaller families at LEI0101 also supported additive effect.

For single-point analysis of association with BW at 37 d of age, three marker loci displayed LOD scores higher than 1.0 (Table 3). The LOD scores for these three loci were 1.48 at MCW0020 (460 cM of chromosome 1), 1.24 at ADL0142 (126 cM of chromosome 6), and 1.31 at ADL0154 (46 cM of chromosome 8), and the heritability due to these loci was 0.15, 0.14, and 0.20, respectively. With multipoint linkage analysis, three LOD score peaks were generated at 484 cM (LOD = 1.65) on chromosome 1, 125 cM (LOD = 1.24) on chromosome 6, and 38 cM (LOD = 1.32) on chromosome 8 (Figure 5). Using the same approach as the analysis of oocyst shedding to identify non-informative families, the LOD scores at these three marker loci increased to 1.94, 2.12, and 1.82, respectively, for single-point analysis if families with zero heritability due to these chromosomal regions were excluded (Table 3). The heritability associated with these loci was also increased by at least 0.06. Multipoint analysis based on these selected families displayed three LOD peaks on chromosomes 1, 6, and 8 with similar LOD scores of 1.89, 2.28, and 1.70, respectively. The LOD score at MCW0058 (241 cM on chromosome 1) that was previously found to link to growth QTL were 1.46 in the single-point analysis (Table 3) and 1.55 in multipoint analysis (Figure 5) based on five families. Thus, no significant growth loci were detected with either single point or multipoint linkage analysis.

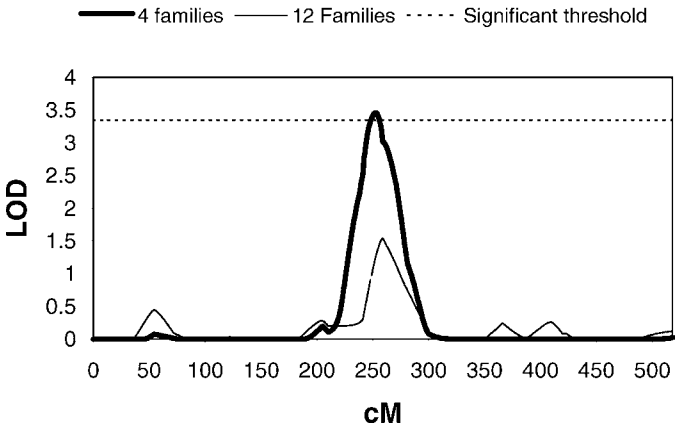

FIGURE 3. The logarithm of odds scores (LOD) of multipoint linkage analysis on chromosome 1 associated with oocyst shedding based on four selected families and 12 families.

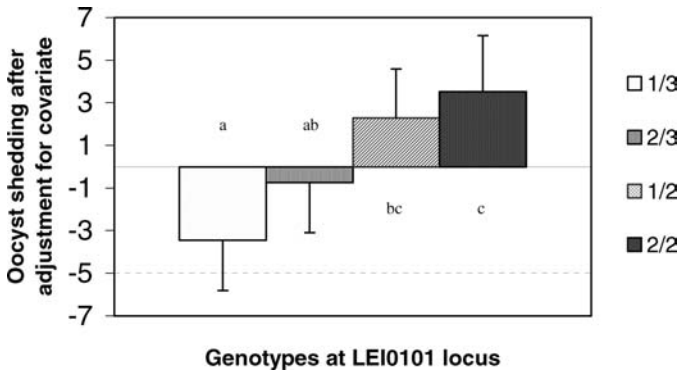

FIGURE 4. The averages of covariate-adjusted oocyst shedding expressed as deviation from the means of four different genotypes at LEI0101 in the family with the most offspring. Error bars indicate standard deviations of the means. [a–c]Means with no common letters were different ($P < 0.05$).

DISCUSSION

In the present study, oocyst shedding was probably the best indicator of resistance to avian coccidiosis. First, this measurement is unique to coccidiosis and it is more relevant to the disease than other parameters. It is generally agreed that birds susceptible to the disease are expected to shed more oocysts PI than those that are resistant. Second, oocyst shedding was independent of both sex and BW at the time of challenge. Third, oocyst shedding displayed the highest correlation with the BW gain after the acute phase of the disease, e.g. from Days 6 to 9 PI. In a previous study, BW gain has also been found to be a good indicator of coccidiosis resistance (Zhu et al., 2000), and high correlation between oocyst shedding and BW gain in the current study confirms the value of oocyst shedding as a phenotypic measurement for resistance to coccidiosis. However, the correlation was not observed in males, possibly due to the significant difference in growth and/or difference in challenging dose per BW between males and females. Male birds gained significantly more weight than females, and the portion of growth reduction due to the disease in males was approximately half of that in females. Males received a smaller challenged dose per Kg of BW than females. Last, oocyst shedding was significantly correlated to the differences in plasma carotenoid concentration between Days 0 and 9 PI in both males and females.

Although the two commercial lines that were crossed to produce the offspring for the current mapping study were previously found to be different in resistance to avian coccidiosis, the individuals chosen from each line may not necessarily differ. In the present study, the individuals that were crossed to produce the F_1 generation were not artificially selected to arrange the mating between susceptible and resistant birds. Therefore, some families may not be informative at the QTL of interest. The QTL detection power may have been significantly increased if non-segregating families were removed, which has been demonstrated with computer simulation by ascertaining samples, selecting families with affected individuals in the genetic analysis (Blangero et al., 2001). For example in the current study, it appeared that eight families were not informative at the QTL close to LEI0101. The heritability due to this locus in the eight families was estimated to be zero. Using this approach to exclude non-informative families, both single-point and multipoint linkage analyses detected a significant QTL associated with oocyst shedding in chromosome 1. However, this approach may increase Type 1 error of the statistic.

Interestingly, the area of the locus associated with oocyst shedding was previously found to affect viremia in chickens infected with Marek's disease virus at the suggestive linkage level with the same marker, LEI0101 (Yonash et al., 1999). These results suggest that a gene(s) in this chromosomal region regulate disease resistance in chickens. Data from current study indicated that the genetic effect due to the detected QTL appeared to be additive based on linkage disequilibrium within the largest families. This result agrees with other genetic estimates based on polygenic models (Champion, 1953; Rosenberg et al., 1953). There were substantial allelic differences at this QTL.

For the growth traits, no significant loci were detected in the present study. The differences among the alleles at growth QTL probably have been reduced a great deal due to long-term artificial selection. More samples are required to detect such genetic effects. The chromosomal region of MCW0058 marker, 20 cM from LEI0101, was previously reported to be suggestively associated with growth in a cross between broiler lines (Van Kaam et al., 1998) and significantly in a cross between Japanese native chickens and broilers (Tatsuda and Fujinaka, 2001). Data of the present experiment also indicated the association. It has been considered that various weak genetic effects of independent studies indicate an overall true genetic affect (Gu et al., 2000); therefore, it is highly possible that there are genes controlling growth in this region.

TABLE 3. The logarithm of odds scores (LOD) at and the heritability due to marker loci based on single-point linkage analysis with body weight at 37 d of age

		All families[1]		Selected families	
Marker loci	Chromosome	LOD	Hq^2	LOD	Hq^2
MCW0058	1	0.54	0.138	1.46	0.273
MCW0020	1	1.48	0.154	1.94	0.215
ADL0142	6	1.24	0.138	2.12	0.232
ADL0154	8	1.31	0.196	1.82	0.280

[1]Hq^2 = heritability due to marker loci.

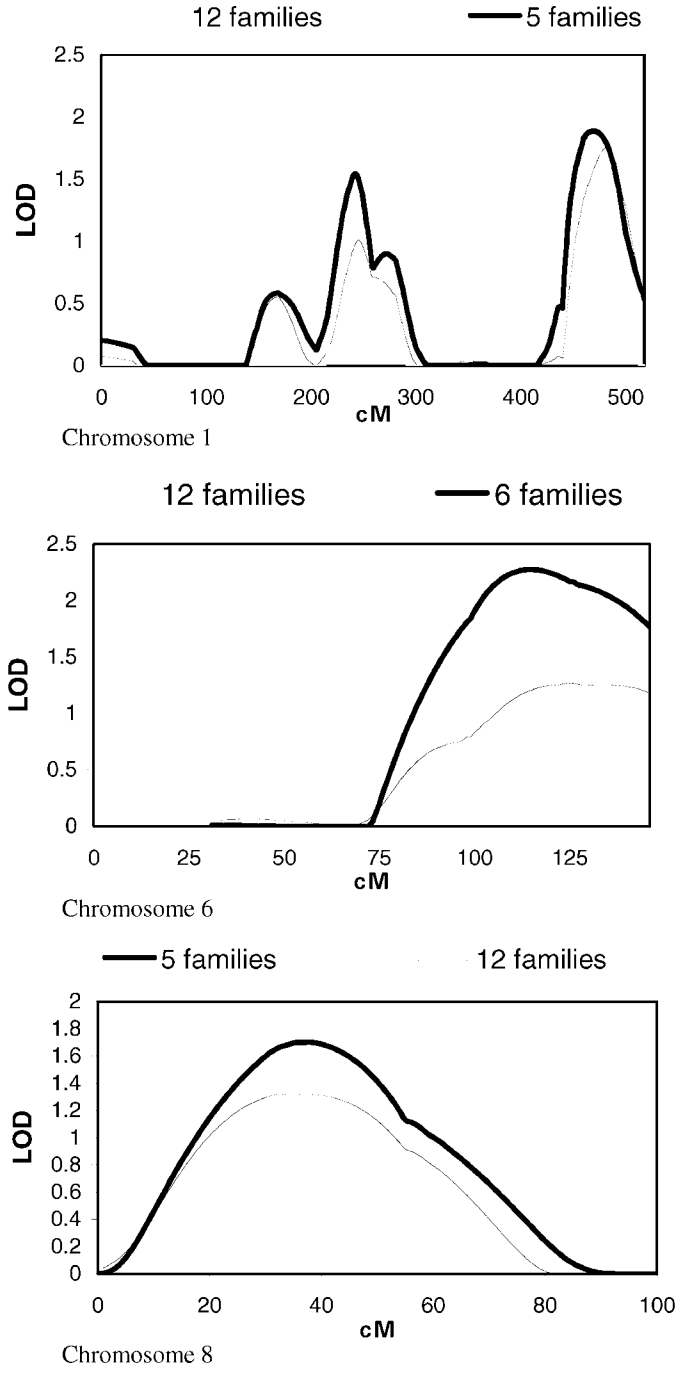

FIGURE 5. The logarithm of odds scores (LOD) of multipoint linkage analysis on chromosomes 1, 6, and 8 associated with chicken body weight at 37 d of age.

In summary, oocyst shedding is a good parameter to measure the status of genetic resistance to coccidiosis caused by *E. maxima*. There is a highly potential QTL close to LEI0101 on chromosome 1 associated with oocyst shedding of *E. maxima*-infected chickens. Replicate experiments and future investigation are needed to verify this QTL for fine mapping to identify the genes involved. Once the susceptible alleles are identified, marker-assistance selection can be applied to select individuals resistant to this disease.

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